

SEQUENCE LISTING	
<110> YAMASHITA, ICHIRO	
<120> High estrogen-sensitive medaka fish	
<130> 210217US-620-7249-0	
<140> US 09/893,666	
<141> 2001-06-29	
<150> JP 2000-247729 <151> 2000-08-17	
<160> 7	
<170> PatentIn version 3.1	
<210> 1	
<211> 2764 <212> DNA	
<213> Oryzias latipes	
<220> <221> CDS	
<221> CDS <222> (211)(1935)	
<223>	
<400> 1	
gtetegetge tagatgeetg teaggeagge agagaggaag cageeegtgt tgegeageae	60
atctgaggat gattcatgag taagagacag agctcggtgc agatcaggca gctgttcgga	120
ccagcactca gatccaggat cagcccagcc tcctcagagc tggagaccct ctccccacct	180
cgcctctcgc cccgtgaccc cctcggtgac atg tac cct gaa gag agc cgg ggt Met Tyr Pro Glu Glu Ser Arg Gly 1 5	234
tct gga ggg gtg gct gct gtg gac ttt ttg gaa ggg acg tac gac tat Ser Gly Gly Val Ala Ala Val Asp Phe Leu Glu Gly Thr Tyr Asp Tyr	282
10 15 20	
gcc gcc ccc aac cct gcc acg act ccc ctt tac agc cag tcc agc acc Ala Ala Pro Asn Pro Ala Thr Thr Pro Leu Tyr Ser Gln Ser Ser Thr	330
25 30 35 40	
ggc tac tac tct gct ccc ctg gaa aca aac gga ccc ccc tca gaa ggc Gly Tyr Tyr Ser Ala Pro Leu Glu Thr Asn Gly Pro Pro Ser Glu Gly	378
45 50 55	
agt ctg cag tcc ctg ggc agt ggg ccg acg agc cct ctg gtg ttt gtg Ser Leu Gln Ser Leu Gly Ser Gly Pro Thr Ser Pro Leu Val Phe Val	426
60 65 70	
ccc tcc agc ccc aga ctc agt ccc ttt atg cat cca ccc agc cac cac	474

Pro	Ser	Ser 75	Pro	Arg	Leu	Ser	Pro 80	Phe	Met	His	Pro	Pro 85	Ser	His	His	
					tcc Ser											522
					cag Gln 110											570
					gga Gly											618
_	_	_		_	gcc Ala		_	_	_		_					666
					tgt Cys											714
	_				gac Asp		_	_					_	_		762
	_	_			agg Arg 190	_	_	_	_	_	_	_			_	810
_		_			atg Met											858
					gac Asp											906
			Lys		cag Gln		His		Thr							954
					gga Gly											1002
					cct Pro 270											1050
					ctc Leu											1098
					atg Met											1146

	300		305	310	
ctg gtc cac Leu Val His 315				Phe Leu	
ctg tcc ctg Leu Ser Leu 330					
gtg ctc atg Val Leu Met 345		u Ile Trp			
ctc atc ttt Leu Ile Phe				 	_
gtg gaa ggc Val Glu Gly		u Ile Phe			
cgc ttc cgt Arg Phe Arg 395				. Cys Leu	
gct att att Ala Ile Ile 410					
atg gag cca Met Glu Pro 425		n Ser Ala			
atc aca gac Ile Thr Asp					
cag gag cag Gln Glu Gln		g Gln Ala			
atc agg cac Ile Arg His 475				Ser Met	
tgc aag aac Cys Lys Asn 490	_		_	 _	•
gcc cac cgc Ala His Arg 505	_	s Pro Val		_	
gtc gac aga Val Asp Arg					

ccc ggt tct ata tca gca tct cga ggc aga atc gag agt ccg agc aga Pro Gly Ser Ile Ser Ala Ser Arg Gly Arg Ile Glu Ser Pro Ser Arg 540 545 550	1866
ggc ccc ttt gct ccc agt gtc ctt cag tat gga ggg tcg cgt cct gac Gly Pro Phe Ala Pro Ser Val Leu Gln Tyr Gly Gly Ser Arg Pro Asp 555 560 565	1914
tgc acc ccg gcc ctt caa gac tgagcacaca gtccaaggcc ctttttttgt Cys Thr Pro Ala Leu Gln Asp 570 575	1965
ggctcaaggg ttcaggttgg gacaaggtga tgcttgattt aattttaaga attatttata	2025
aataagagtg gcgctgagag gagaagctcc cacaatgaac tgcctctgct tggtccagct	2085
tttgtgcagt cactttaatc tgcttatatt catctccttt gtaaacctga gcgtctcttt	2145
agcagetttt ttttgetete caaacageat gtggtagatt gtaaggttge gteecatgag	2205
ttctggtgat ttcaagaaaa tgagcagcta atgttttctg taaccgtctt gacccaagtg	2265
cactteetet tggattaaag gggetaatgg geattatttt gtetettgta catatgggat	2325
ggctaagaat aatgagagta attgtcagat tttgtgtaga acttacccac aaatgcaatt	2385
ttaaaataag atttaaaaac aaaagaggca agatcaaacc tgagagcact gaagacacgc	2445
tgtagaaagc tgggtaaatt tgttatccac gtctatctct ggaaaggact ttgttctctg	2505
tgcctgcagc tcatttactc tgaacttgct acttgttgaa catttgtgca cttgtccgtg	2565
tttttctagc actgtagctt atgaacgctg agaaagaatc taatgctttg atgcacagat	2625
ttgccttgta ttgtacatct cagccacaaa cgtacttttc gtccacaagt tgactgactg	2685
caccttgatt aaattgtcta aaagttcatt taaatgttga attctgtgaa aattaaaaag	2745
gcaattcctg tttctattt	2764

<210> 2

<211> 575

<212> PRT

<213> Oryzias latipes

<400> 2

Met Tyr Pro Glu Glu Ser Arg Gly Ser Gly Gly Val Ala Ala Val Asp 1 5 10 15

Phe Leu Glu Gly Thr Tyr Asp Tyr Ala Ala Pro Asn Pro Ala Thr Thr 20 25 30

Pro Leu Tyr Ser Gln Ser Ser Thr Gly Tyr Tyr Ser Ala Pro Leu Glu 35 40 45

Thr Asn Gly Pro Pro Ser Glu Gly Ser Leu Gln Ser Leu Gly Ser Gly 50 55 60

Pro Thr Ser Pro Leu Val Phe Val Pro Ser Ser Pro Arg Leu Ser Pro 65 70 75 80

Phe Met His Pro Pro Ser His His Tyr Leu Glu Thr Thr Ser Thr Pro 85 90 95

Val Tyr Arg Ser Ser His Gln Gly Ala Ser Arg Glu Asp Gln Cys Gly
100 105 110

Ser Arg Glu Asp Thr Cys Ser Leu Gly Glu Leu Gly Ala Gly Ala Gly 115 120 125

Ala Gly Gly Phe Glu Met Ala Lys Asp Thr Arg Phe Cys Ala Val Cys 130 135 140

Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly 145 150 155 160

Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met 165 170 175

Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg Asn Arg Arg Lys Ser 180 185 190

Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys 195 200 205

Gly Gly Val Arg Lys Asp Arg Ile Arg Ile Leu Arg Arg Asp Lys Arg 210 215 220

Arg Thr Gly Val Gly Asp Gly Asp Lys Val Val Lys Gly Gln Glu His 225 230 235

Lys Thr Val His Tyr Asp Gly Arg Lys Arg Ser Ser Thr Gly Gly Gly 245 250 255

Gly Gly Gly Gly Gly Arg Leu Ser Val Thr Ser Ile Pro Pro Glu

260 265 270

Gln Val Leu Leu Leu Gln Gly Ala Glu Pro Pro Ile Leu Cys Ser 275 280 285

Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val Thr Met Met Thr Leu 290 295 300

Leu Thr Ser Met Ala Asp Lys Glu Leu Val His Met Ile Ala Trp Ala 305 310 315

Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu His Asp Gln Val Leu 325 330 335

Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met Ile Gly Leu Ile Trp 340 345 350

Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe Ala Gln Asp Leu Ile 355 360 365

Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly Met Thr Glu Ile Phe 370 375 380

Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Val Leu Lys Leu Lys 385 390 395 400

Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu Leu Asn Ser Gly 405 410 415

Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu His Asn Ser Ala 420 425 430

Ala Val Gln Ser Met Leu Asp Thr Ile Thr Asp Ala Leu Ile His Tyr 435 440 445

Ile Ser Gln Ser Gly Tyr Leu Ala Gln Glu Gln Ala Arg Arg Gln Ala 450 455 460

Gln Leu Leu Leu Leu Ser His Ile Arg His Met Ser Asn Lys Gly 465 470 475 480

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys Val Pro Leu Tyr 485 490 495

Asp	Leu	Leu	Leu 500	Glu	Met	Leu	Asp	Ala 505	His	Arg	Leu	His	His 510	Pro	Val	
Arg	Ala	Pro 515	Gln	Ser	Leu	Ser	Gln 520	Val	Asp	Arg	Asp	Pro 525	Pro	Ser	Thr	
Ser	Ser 530	Gly	Gly	Gly	Gly	Ile 535	Ala	Pro	Gly	Ser	Ile 540	Ser	Ala	Ser	Arg	
Gly 545	Arg	Ile	Glu	Ser	Pro 550	Ser	Arg	Gly	Pro	Phe 555	Ala	Pro	Ser	Val	Leu 560	
Gln	Tyr	Gly	Gly	Ser 565	Arg	Pro	Asp	Cys	Thr 570	Pro	Ala	Leu	Gln	Asp 575		
<210> 3 <211> 20 <212> DNA <213> ARTIFICIAL SEQUENCE																
<22 <22 <40	3>	SYNT														20
tcg	gtga	cat	gtac	ccts	jaa											20
<21 <21		4 20														
		DNA ARTI	FIC	(AL S	SEQUE	ENCE										
	20> 23>	SYNT	THET:	IC DI	AV											
	00> gtgt	4 gctc	agto	cttg	aag											20
<2 <2	10> 11> 12> 13>	5 20 DNA ART		IAL	SEQU	ENCE										
	20> 23>	SYN	THET	IC D	NA											

20

<400> 5

cttccgtgtg ctcaaactca

<210>	6	
<211>	20	
<212>	DNA	
<213>	ARTIFICIAL DNA	
400		
<400>		20
gtagga	ggtc ataaagaggg	
<210>	7	
<211>	20	
<212>	DNA	
<213>	ARTIFICIAL SEQUENCE	
<220>		
<223>	SYNTHETIC DNA	
<400>		20
gaggga	cttt gttcttgcac	